

In order to avoid security-related warning messages when switching to secured connection, you may want either to:

- confirm the exception on the next page, or
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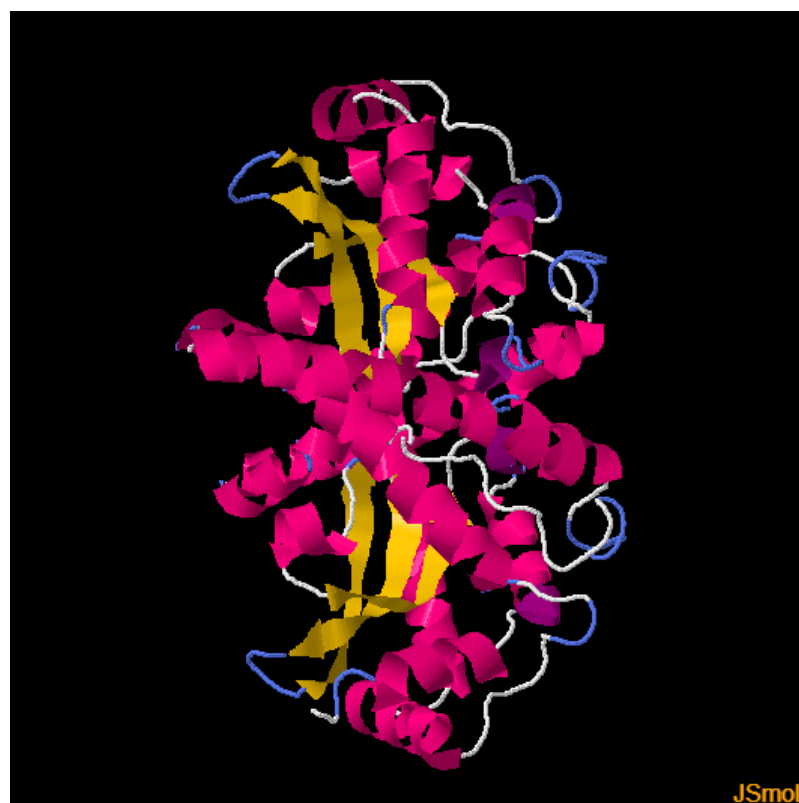
SwissDock

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Predicted binding modes for your request Quercetinsoddock

This page remains accessible one week after the docking completion. - [review parameters](#)

The [SwissDock forum](#) can help you understand the docking outcome.



Show	Cluster	Element	FullFitness (kcal/mol)	Estimated ΔG (kcal/mol)
<input type="radio"/>	0	0	-1880.43	-8.20
<input type="radio"/>	0	1	-1879.08	-7.97
<input checked="" type="radio"/>	0	2	-1871.48	-7.31
<input type="radio"/>	0	3	-1870.86	-7.33
<input type="radio"/>	0	4	-1870.81	-7.38
<input type="radio"/>	0	5	-1868.86	-7.37
<input type="radio"/>	0	6	-1865.51	-7.36
<input type="radio"/>	1	0	-1878.87	-6.56
<input type="radio"/>	1	1	-1878.65	-6.54
<input type="radio"/>	1	2	-1878.25	-6.53
<input type="radio"/>	1	3	-1878.21	-6.53
<input type="radio"/>	1	4	-1876.13	-6.30
<input type="radio"/>	1	5	-1874.69	-6.44
<input type="radio"/>	1	6	-1874.61	-6.41
<input type="radio"/>	1	7	-1874.22	-6.56
<input type="radio"/>	2	0	-1878.77	-7.27
<input type="radio"/>	2	1	-1877.53	-7.17
<input type="radio"/>	2	2	-1877.47	-7.17
<input type="radio"/>	2	3	-1875.99	-6.87
<input type="radio"/>	2	4	-1875.51	-6.59
<input type="radio"/>	2	5	-1874.55	-6.64
<input type="radio"/>	2	6	-1874.54	-6.65

[Download CSV file](#)

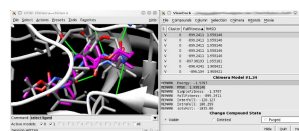
If predicted binding modes are not displayed, you might suffer from a Jsmol bug we are investigating. In the meantime, please use UCSF Chimera (see below).

Binding modes are scored using their FullFitness and clustered. Clusters are then ranked according to the average FullFitness of their elements (see [Grosdidier et. al., Proteins. 2007 Jun 1;67\(4\):1010-25.](#))

For further inspection, you can either download predictions files, or open UCSF Chimera from your browser:



[Download your predictions file](#)



[Launch UCSF Chimera to visualize predicted binding modes](#)
 You can get Chimera [here](#). Your browser must be [properly configured](#).

Help us improve SwissDock by telling us

Help us improve SWISSDOCK by telling us more about you

This survey is not mandatory. If you choose to answer it, please do it only once.

* Required

What is your email address? *

Your answer

What is your background? *

- Biology
- Chemistry
- Physics
- MD
- PharmD
- Other:

What best describes your current position? *

- Student
- PhD
- Post-Doc
- Permanent position
- Professor
- Other:

What are you using SwissDock for? *

- Creating pictures
- Testing hypotheses
- Finding active compounds
- Other:

Which molecular viewer are you familiar with? *

- UCSF Chimera
- PyMol

—

 VMD Other:

Are you familiar with scripting (bash, perl, etc...)? *

 No

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